

016405-8.ST25.txt
SEQUENCE LISTING

<110> BAROJA FERNANDEZ, Miren Edurne
MUNOZ PEREZ, Francisco Jose
POZUETA ROMERO, Francisco Javier
MORAN ZORZANO, Maria Teresa
ALONSO CASAJUS, Nora

<120> METHOD OF PRODUCTION OF RECOMBINANT SUCROSE SYNTHASE, USE
THEREOF IN THE MANUFACTURE OF KITS FOR DETERMINATION OF SUCROSE,
PRODUCTION OF ADPGLUCOSE AND PRODUCTION OF TRANSGENIC PLANTS
WHOSE LEAVES AND STORAGE ORGANS ACCUMULATE HIGH CONTENTS OF
ADPGLUCOSE AND STARCH

<130> U 016405-8

<140> 10/587,372
<141> 2008-06-12

<160> 12

<170> PatentIn version 3.3

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<212> DNA
<213> Solanum tuberosum

<220>
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<213> Solanum tuberosum

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| cccccttggg ttgcacttgc tattcgtttg aggcctggtg tctgggaata catccgtgtg | 300 |
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| catctgtgtg tgctcaagga caggactaaa ccaattttat tcacaatggc aaggttggat | 1740 |
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<210> 4
 <211> 841
 <212> PRT
 <213> Solanum tuberosum

<220>
 <223> SSX fused with a histidine-rich amino acid tail deducted after expression of SSX in the PET-28a(+) expression plasmid

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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
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Gly Ser Glu Phe Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu
 35 40 45

Arg Glu Arg Val Asp Ala Thr Leu Ala Ala His Arg Asn Glu Ile Leu
 50 55 60

Leu Phe Leu Ser Arg Ile Glu Ser His Gly Lys Gly Ile Leu Lys Pro
 65 70 75 80

His Glu Leu Leu Ala Glu Phe Asp Ala Ile Arg Gln Asp Asp Lys Asn
 85 90 95

Lys Leu Asn Glu His Ala Phe Glu Glu Leu Leu Lys Ser Thr Gln Glu
 100 105 110

Ala Ile Val Leu Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro
 115 120 125

Gly Val Trp Glu Tyr Ile Arg Val Asn Val Asn Ala Leu Val Val Glu
 130 135 140

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Gly Ala Ser Asn Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
165 170 175

Thr Ala Ser Phe Pro Lys Pro Thr Leu Thr Lys Ser Ile Gly Asn Gly
180 185 190

Val Glu Phe Leu Asn Arg His Leu Ser Ala Lys Met Phe His Asp Lys
195 200 205

Glu Ser Met Thr Pro Leu Leu Glu Phe Leu Arg Ala His His Tyr Lys
210 215 220

Gly Lys Thr Met Met Leu Asn Asp Arg Ile Gln Asn Ser Asn Thr Leu
225 230 235 240

Gln Asn Val Leu Arg Lys Ala Glu Glu Tyr Leu Ile Met Leu Ser Pro
245 250 255

Asp Thr Pro Tyr Phe Glu Phe Glu His Lys Phe Gln Glu Ile Gly Leu
260 265 270

Glu Lys Gly Trp Gly Asp Thr Ala Glu Arg Val Leu Glu Met Val Cys
275 280 285

Met Leu Leu Asp Leu Leu Glu Ala Pro Asp Ser Cys Thr Leu Glu Lys
290 295 300

Phe Leu Gly Arg Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
305 310 315 320

His Gly Tyr Phe Ala Gln Glu Asn Val Leu Gly Tyr Pro Asp Thr Gly
325 330 335

Gly Gln Val Val Tyr Ile Leu Asp Gln Val Pro Ala Leu Glu Arg Glu
340 345 350

Met Leu Lys Arg Ile Lys Glu Gln Gly Leu Asp Ile Ile Pro Arg Ile
355 360 365

Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly
370 375 380

Gln Arg Ile Glu Lys Val Tyr Gly Ala Glu His Ser His Ile Leu Arg
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Val Pro Phe Arg Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg
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Phe Glu Val Trp Pro Tyr Met Glu Thr Phe Ile Glu Asp Val Ala Lys
420 425 430

Glu Ile Ser Ala Glu Leu Gln Ala Lys Pro Asp Leu Ile Ile Gly Asn
435 440 445

Tyr Ser Glu Gly Asn Leu Ala Ala Ser Leu Leu Ala His Lys Leu Gly
450 455 460

Val Thr Gln Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
465 470 475 480

Asp Ser Asp Ile Tyr Trp Lys Lys Phe Asp Glu Lys Tyr His Phe Ser
485 490 495

Ser Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile
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Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly
515 520 525

Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg Val
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Gly Ala Asp Ile Asn Leu Tyr Phe Ser Tyr Ser Glu Thr Glu Lys Arg
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Glu Asn Asp Glu His Leu Cys Val Leu Lys Asp Arg Thr Lys Pro Ile
595 600 605

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610 615 620

Val Glu Trp Tyr Ala Lys Asn Pro Arg Leu Arg Gly Leu Val Asn Leu
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Val Val Val Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu

Gln Ala Glu Met Lys Lys Met Tyr Glu Leu Ile Glu Thr His Asn Leu
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Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr Lys Gly Ala Phe Val Gln
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Cys Gly Leu Pro Thr Phe Ala Thr Asn His Gly Gly Pro Ala Glu Ile
725 730 735

Ile Val His Gly Lys Ser Gly Phe His Ile Asp Pro Tyr His Gly Glu
740 745 750

Gln Ala Ala Asp Leu Leu Ala Asp Phe Phe Glu Lys Cys Lys Lys Glu
755 760 765

Pro Ser His Trp Glu Thr Ile Ser Thr Gly Gly Leu Lys Arg Ile Gln
770 775 780

Glu Lys Tyr Thr Trp Gln Ile Tyr Ser Glu Arg Leu Leu Thr Leu Ala
785 790 795 800

Ala Val Tyr Gly Phe Trp Lys His Val Ser Lys Leu Asp Arg Leu Glu
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Ala Glu Ala Val Pro Leu Ala Ala Glu
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<213> Solanum tuberosum

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<210> 6
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 <212> DNA
 <213> Solanum tuberosum

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 <223> "Reverse" promoter required for the point mutagenesis of SSX

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 <211> 42
 <212> DNA
 <213> Solanum tuberosum

<220>
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<210> 8
 <211> 42
 <212> DNA
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<220>
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 <212> DNA
 <213> Solanum tuberosum

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 <223> "Forward" promoter required for point mutagenesis of SSX and
 production of SS5

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 <213> Solanum tuberosum

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<223> "Reverse" promoter required for point mutagenesis of SSX and production of SS5

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 <213> Solanum tuberosum

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 20 25 30

Gly Ser Glu Phe Met Ala Glu Arg Val Leu Thr Arg Val His Ser Leu
 35 40 45

Arg Glu Arg Val Asp Ala Thr Leu Ala Ala His Arg Asn Glu Ile Leu
 Page 9

50

55

60

Leu Phe Leu Ser Arg Ile Glu Ser His Gly Lys Gly Ile Leu Lys Pro
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His Glu Leu Leu Ala Glu Phe Asp Ala Ile Arg Gln Asp Asp Lys Asn
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Lys Leu Asn Glu His Ala Phe Glu Glu Pro Leu Lys Ser Thr Gln Glu
100 105 110

Ala Ile Val Leu Pro Pro Trp Val Ala Leu Ala Ile Arg Leu Arg Pro
115 120 125

Gly Val Trp Glu Tyr Ile Arg Val Asn Val Asn Ala Leu Val Val Glu
130 135 140

Glu Leu Ser Val Pro Glu Tyr Leu Gln Phe Lys Glu Glu Leu Val Asp
145 150 155 160

Gly Ala Ser Asn Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe
165 170 175

Thr Ala Ser Phe Pro Lys Pro Thr Leu Thr Lys Ser Ile Gly Asn Gly
180 185 190

Val Glu Phe Leu Asn Arg His Leu Ser Ala Lys Met Phe His Asp Lys
195 200 205

Glu Ser Met Thr Pro Leu Leu Glu Phe Leu Arg Ala His His Tyr Lys
210 215 220

Gly Lys Thr Met Met Leu Asn Asp Arg Ile Gln Asn Ser Asn Thr Leu
225 230 235 240

Gln Asn Val Leu Arg Lys Ala Glu Glu Tyr Leu Ile Met Leu Ser Pro
245 250 255

Asp Thr Pro Tyr Phe Glu Phe Glu His Lys Phe Gln Glu Ile Gly Leu
260 265 270

Glu Lys Gly Trp Gly Asp Thr Ala Glu Arg Val Leu Glu Met Val Cys
275 280 285

Met Leu Leu Asp Leu Leu Glu Ala Pro Asp Ser Cys Thr Leu Glu Lys
290 295 300

Phe Leu Gly Arg Ile Pro Met Val Phe Asn Val Val Ile Leu Ser Pro
 305 310 315 320

His Gly Tyr Phe Ala Gln Glu Asn Val Leu Gly Tyr Pro Asp Thr Gly
 325 330 335

Gly Gln Val Val Tyr Ile Leu Asp Gln Val Pro Ala Leu Glu Arg Glu
 340 345 350

Met Leu Lys Arg Ile Lys Glu Gln Gly Leu Asp Ile Ile Pro Arg Ile
 355 360 365

Leu Ile Val Thr Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly
 370 375 380

Gln Arg Ile Glu Lys Val Tyr Gly Ala Glu His Ser His Ile Leu Arg
 385 390 395 400

Val Pro Phe Arg Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg
 405 410 415

Phe Glu Val Trp Pro Tyr Met Glu Thr Phe Ile Glu Asp Val Ala Lys
 420 425 430

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 435 440 445

Tyr Ser Glu Gly Asn Leu Ala Ala Ser Leu Leu Ala His Lys Leu Gly
 450 455 460

Val Thr Gln Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro
 465 470 475 480

Asp Ser Asp Ile Tyr Trp Lys Lys Phe Asp Glu Lys Tyr His Phe Ser
 485 490 495

Ser Gln Phe Thr Ala Asp Leu Ile Ala Met Asn His Thr Asp Phe Ile
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Ile Thr Ser Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly
 515 520 525

Gln Tyr Glu Ser His Met Ala Phe Thr Met Pro Gly Leu Tyr Arg Val
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Gly Ala Asp Ile Asn Leu Tyr Phe Ser Tyr Ser Glu Thr Glu Lys Arg
565 570 575

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580 585 590

Glu Asn Asp Glu His Leu Cys Val Leu Lys Asp Arg Thr Lys Pro Ile
595 600 605

Leu Phe Thr Met Ala Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu
610 615 620

Val Glu Trp Tyr Ala Lys Asn Pro Arg Leu Arg Gly Leu Val Asn Leu
625 630 635 640

Val Val Val Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu
645 650 655

Gln Ala Glu Met Lys Lys Met Tyr Glu Leu Ile Glu Thr His Asn Leu
660 665 670

Asn Gly Gln Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Val Arg Asn
675 680 685

Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr Lys Gly Ala Phe Val Gln
690 695 700

Pro Ala Phe Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr
705 710 715 720

Cys Gly Leu Pro Thr Phe Ala Thr Asn His Gly Gly Pro Ala Glu Ile
725 730 735

Ile Val His Gly Lys Ser Gly Phe His Ile Asp Pro Tyr His Gly Glu
740 745 750

Gln Ala Ala Asp Leu Leu Ala Asp Phe Phe Glu Lys Cys Lys Arg Glu
755 760 765

Pro Ser His Trp Glu Thr Ile Ser Thr Asp Gly Leu Lys Arg Ile Gln
770 775 780

Glu Lys Tyr Thr Trp Gln Ile Tyr Ser Glu Arg Leu Leu Thr Leu Ala
785 790 795 800

Ala Val Tyr Gly Phe Trp Lys His Val Ser Lys Leu Asp Arg Leu Glu
805 810 815

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Ile Arg Arg Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Met
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Ala Glu Ala Val Pro Leu Ala Ala Glu
835 840